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```
  1 GNTCTAGAANTA GTGGATCCCCCC GGGCTGCAGGAA TTCCGACGGCCC CTGGAAGGGCTC TGGTGGGGCTGA
    CNAGATCTTNAT CACCTAGGGGGG CCCGACGTCCTT AAGGCTGCCGGG GACCTTCCCGAG ACCACCCCGACT

 73 GCGCTCTGCCGC GGGGGCGCGGGC ACAGCAGGAAGC AGGTCCGCGTGG GCGCTGGGGGCA TCAGCTACCGGG
    CGCGAGACGGCG CCCCCGCGCCCG TGTCGTCCTTCG TCCAGGCGCACC CGCGACCCCCGT AGTCGATGGCCC

145 GTGGTCCGGGCT GAAGAGCCAGGC AGCCAAGGCAGC CACCCCGGGGGG TGGGCGACTTTG GGGGAGTTGGTG
    CACCAGGCCCGA CTTCTCGGTCCG TCGGTTCCGTCG GTGGGGCCCCCC ACCCGCTGAAAC CCCCTCAACCAC

217 CCCCGCCCCCCA GGCCTTGGCGGG GTCATGGGGCCC CCCCATTCTGGG CCGGGGGGCGTG CGAGTCGGGGCC
    GGGGCGGGGGGT CCGGAACCGCCC CAGTACCCCGGG GGGGTAAGACCC GGCCCCCCGCAC GCTCAGCCCCGG
  1                               MetGlyPro ProHisSerGly ProGlyGlyVal ArgValGlyAla

289 CTGCTGCTGCTG GGGGTTTTGGGG CTGGTGTCTGGG CTCAGCCTGGAG CCTGTCTACTGG AACTCGGCGAAT
    GACGACGACGAC CCCCAAAACCCC GACCACAGACCC GAGTCGGACCTC GGACAGATGACC TTGAGCCGCTTA
 16 LeuLeuLeuLeu GlyValLeuGly LeuValSerGly LeuSerLeuGlu ProValTyrTrp AsnSerAlaAsn

361 AAGAGGTTCCAG GCAGAGGGTGGT TATGTGCTGTAC CCTCAGATCGGG GACCGGCTAGAC CTGCTCTGCCCC
    TTCTCCAAGGTC CGTCTCCCACCA ATACACGACATG GGAGTCTAGCCC CTGGCCGATCTG GACGAGACGGGG
 40 LysArgPheGln AlaGluGlyGly TyrValLeuTyr ProGlnIleGly AspArgLeuAsp LeuLeuCysPro

433 CGGGCCCGGCCT CCTGGCCCTCAC TCCTCTCCTAAT TATGAGTTCTAC AAGCTGTACCTG GTAGGGGGTGCT
    GCCCGGGCCGGA GGACCGGGAGTG AGGAGAGGATTA ATACTCAAGATG TTCGACATGGAC CATCCCCCACGA
 64 ArgAlaArgPro ProGlyProHis SerSerProAsn TryGluPheTyr LysLeuTyrLeu ValGlyGlyAla

505 CAGGGCCGGCGC TGTGAGGCACCC CCTGCCCCAAAC CTCCTTCTCACT TGTGATCGCCCA GACCTGGATCTC
    GTCCCGGCCGCG ACACTCCGTGGG GGACGGGGTTTG GAGGAAGAGTGA ACACTAGCGGGT CTGGACCTAGAG
 88 GlnGlyArgArg CysGluAlaPro ProAlaProAsn LeuLeuLeuThr CysAspArgPro AspLeuAspLeu

577 CGCTTCACCATC AAGTTCCAGGAG TATAGCCCTAAT CTCTGGGGCCAC GAGTTCCGCTCG CACCACGATTAC
    GCGAAGTGGTAG TTCAAGGTCCTC ATATCGGGATTA GAGACCCCGGTG CTCAAGGCGAGC GTGGTGCTAATG
112 ArgPheThrIle LysPheGlnGlu TyrSerProAsn LeuTrpGlyHis GluPheArgSer HisHisAspTyr
```

FIG. 1A

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649  TACATCATTGCC ACATCGGATGGG ACCCGGGAGGGC CTGGAGAGCCTG CAGGGAGGTGTG TGCCTAACCAGA
     ATGTAGTAACGG TGTAGCCTACCC TGGGCCCTCCCG GACCTCTCGGAC GTCCCTCCACAC ACGGATTGGTCT
136  TyrIleIleAla ThrSerAspGly ThrArgGluGly LeuGluSerLeu GlnGlyGlyVal CysLeuThrArg

721  GGCATGAAGGTG CTTCTCCGAGTG GGACAAAGTCCC CGAGGAGGGGCT GTCCCCCGAAAA CCTGTGTCTGAA
     CCGTACTTCCAC GAAGAGGCTCAC CCTGTTTCAGGG GCTCCTCCCCGA CAGGGGCTTTT GGACACAGACTT
160  GlyMetLysVal LeuLeuArgVal GlyGlnSerPro ArgGlyGlyAla ValProArgLys ProValSerGlu

793  ATGCCCATGGAA AGAGACCGAGGG GCAGCCCACAGC CTGGAGCCTGGG AAGGAGAACCTG CCAGGTGACCCC
     TACGGGTACCTT TCTCTGGCTCCC CGTCGGGTGTCG GACCTCGGACCC TTCCTCTTGGAC GGTCCACTGGGG
184  MetProMetGlu ArgAspArgGly AlaAlaHisSer LeuGluProGly LysGluAsnLeu ProGlyAspPro

865  ACCAGCAATGCA ACCTCCCGGGGT GCTGAAGGCCCC CTGCCCCCTCCC AGCATGCCTGCA GTGGCTGGGGCA
     TGGTCGTTACGT TGGAGGGCCCCA CGACTTCCGGGG GACGGGGGAGGG TCGTACGGACGT CACCGACCCCGT
208  ThrSerAsnAla ThrSerArgGly AlaGluGlyPro LeuProProPro SerMetProAla ValAlaGlyAla

937  GCAGGGGGGCTG GCGCTGCTCTTG CTGGGCGTGGCA GGGGCTGGGGGT GCCATGTGTTGG CGGAGACGGCGG
     CGTCCCCCCGAC CGCGACGAGAAC GACCCGCACCGT CCCCGACCCCCA CGGTACACAACC GCCTCTGCCGCC
232  AlaGlyGlyLeu AlaLeuLeuLeu LeuGlyValAla GlyAlaGlyGly AlaMetCysTrp ArgArgArgArg

1009 GCCAAGCCTTCG GAGAGTCGCCAC CCTGGTCCTGGC TCCTTCGGGAGG GGAGGGTCTCTG GGCCTGGGGGGT
     CGGTTCGGAAGC CTCTCAGCGGTG GGACCAGGACCG AGGAAGCCCTCC CCTCCCAGAGAC CCGGACCCCCCA
256  AlaLysProSer GluSerArgHis ProGlyProGly SerPheGlyArg GlyGlySerLeu GlyLeuGlyGly

1081 GGAGGTGGGATG GGACCTCGGGAG GCTGAGCCTGGG GAGCTAGGGATA GCTCTGCGGGGT GGCGGGGCTGCA
     CCTCCACCCTAC CCTGGAGCCCTC CGACTCGGACCC CTCGATCCCTAT CGAGACGCCCCA CCGCCCCGACGT
280  GlyGlyGlyMet GlyProArgGlu AlaGluProGly GluLeuGlyIle AlaLeuArgGly GlyGlyAlaAla

1153 GATCCCCCCTTC TGCCCCCACTAT GAGAAGGTGAGT GGTGACTATGGG CATCCTGTGTAT ATCGTGCAGGAT
     CTAGGGGGGAAG ACGGGGGTGATA CTCTTCCACTCA CCACTGATACCC GTAGGACACATA TAGCACGTCCTA
304  AspProProPhe CysProHisTyr GluLysValSer GlyAspTyrGly HisProValTyr IleValGlnAsp

1225 GGGCCCCCCCAG AGCCCTCCAAAC ATCTACTACACA TCGATTTCTGTG TTGGAGTGGCCC ATATTGCATACG
     CCCGGGGGGGTC TCGGGAGGTTTG TAGATGATGTGT AGCTAAAGACAC AACCTCACCGGG TATAACGTATGC
328  GlyProProGln SerProProAsn IleTyrTyrThr SerIleSerVal LeuGluTrpPro IleLeuHisThr
```

FIG. 1B

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1297 ATACAACTGTTT TTCATGCGATCC AAGTGCTCCCGT GTCACTACATTC TTATTTCCTGTG CAAGTTATTACG
     TATGTTGACAAA AAGTACGCTAGG TTCACGAGGGCA CAGTGATGTAAG AATAAAGGACAC GTTCAATAATGC
 352 IleGlnLeuPhe PheMetArgSer LysCysSerArg ValThrThrPhe LeuPheProVal GlnValIleThr

1369 ACATCGACTTGC CGGATGACTTCA TTTAGCTTTACC ACCCTGAACCCA TCCATGCAGGCC TGCAGAGCACAG
     TGTAGCTGAACG GCCTACTGAAGT AAATCGAAATGG TGGGACTTGGGT AGGTACGTCCGG ACGTCTCGTGTC
 376 ThrSerThyCys ArgMetThrSer PheSerPheThr ThrLeuAsnPro SerMetGlnAla CysArgAlaGln

1441 ATGGGGGAATTC CGAATCAGATGG TGTTTCTGGGGG GACAGGATCCTG GGTACGGCTCTG TTTGTGCTTGTG
     TACCCCCTTAAG GCTTAGTCTACC ACAAAGACCCCC CTGTCCTAGGAC CCATGCCGAGAC AAACACGAACAC
 400 MetGlyGluPhe ArgIleArgTrp CysPheTrpGly AspArgIleLeu GlyThrAlaLeu PheValLeuVal

1513 CTTATTCTTCTT CTTGGGAGGCTG AATATGCATCAG ACGACACTGCTC CGGCAACGGGCC AGTGTGGAGGCG
     GAATAAGAAGAA GAACCCTCCGAC TTATACGTAGTC TGCTGTGACGAG GCCGTTGCCCGG TCACACCTCCGC
 424 LeuIleLeuLeu LeuGlyArgLeu AsnMetHisGln ThrThrLeuLeu ArgGlnArgAla SerValGluAla

1585 GAAGCCGGCCAG CATGGTCCCCTG TGATAGGATTGA AAGAGCTACTGA GAATAGGGGGCT TCTCAATGAGAG
     CTTCGGCCGGTC GTACCAGGGGAC ACTATCCTAACT TTCTCGATGACT CTTATCCCCCGA AGAGTTACTCTC
 448 GluAlaGlyGln HisGlyProLeu (SEQ ID NO: 2)

1657 AGCGGAGGCTGC TGTTATCATGGG AACCAGGCAGAT CAATCATCCCTG GCAGGTCAGGCA GGAAGTTACTTA
     TCGCCTCCGACG ACAATAGTACCC TTGGTCCGTCTA GTTAGTAGGGAC CGTCCAGTCCGT CCTTCAATGAAT

1729 GCTTCTCCTTCA CCTTCTTCCCAC AGAATTTATTAT AGGCTTGTTCCA AGTTGTAGTGTG TGATCAGATTCG
     CGAAGAGGAAGT GGAAGAAGGGTG TCTTAAATAATA TCCGAACAAGGT TCAACATCACAC ACTAGTCTAAGC

1801 TGCTGCCTGTCA GCTCTGTGCTAC CTGGCAGTTCCC CTCATGGAATTC GATATCAAGCTT ATCGATACCGTC
     ACGACGGACAGT CGAGACACGATG GACCGTCAAGGG GAGTACCTTAAG CTATAGTTCGAA TAGCTATGGCAG

1873 GACCT (SEQ ID NO: 1)
     CTGGA
```

FIG. 1C

FIG. 1A
FIG. 1B
FIG. 1C

FIG. 1

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  1 GNTCTAGAANTA GTGGATCCCCCC GGGCTGCAGGAA TTCCGACGGCCC CTGGAAGGGCTC TGGTGGGGCTGA
    CNAGATCTTNAT CACCTAGGGGGG CCCGACGTCCTT AAGGCTGCCGGG GACCTTCCCGAG ACCACCCCGACT

 73 GCGCTCTGCCGC GGGGGCGCGGGC ACAGCAGGAAGC AGGTCCGCGTGG GCGCTGGGGGCA TCAGCTACCGGG
    CGCGAGACGGCG CCCCCGCGCCCG TGTCGTCCTTCG TCCAGGCGCACC CGCGACCCCCGT AGTCGATGGCCC

145 GTGGTCCGGGCT GAAGAGCCAGGC AGCCAAGGCAGC CACCCCGGGGGG TGGGCGACTTTG GGGGAGTTGGTG
    CACCAGGCCCGA CTTCTCGGTCCG TCGGTTCCGTCG GTGGGGCCCCCC ACCCGCTGAAAC CCCCTCAACCAC

217 CCCCGCCCCCCA GGCCTTGGCGGG GTCATGGGGCCC CCCCATTCTGGG CCGGGGGGCGTG CGAGTCGGGGCC
    GGGGCGGGGGGT CCGGAACCGCCC CAGTACCCCGGG GGGGTAAGACCC GGCCCCCCGCAC GCTCAGCCCCGG
  1                              MetGlyPro ProHisSerGly ProGlyGlyVal ArgValGlyAla

289 CTGCTGCTGCTG GGGGTTTTGGGG CTGGTGTCTGGG CTCAGCCTGGAG CCTGTCTACTGG AACTCGGCGAAT
    GACGACGACGAC CCCCAAAACCCC GACCACAGACCC GAGTCGGACCTC GGACAGATGACC TTGAGCCGCTTA
 16 LeuLeuLeuLeu GlyValLeuGly LeuValSerGly LeuSerLeuGlu ProValTyrTrp AsnSerAlaAsn

361 AAGAGGTTCCAG GCAGAGGGTGGT TATGTGCTGTAC CCTCAGATCGGG GACCGGCTAGAC CTGCTCTGCCCC
    TTCTCCAAGGTC CGTCTCCCACCA ATACACGACATG GGAGTCTAGCCC CTGGCCGATCTG GACGAGACGGGG
 40 LysArgPheGln AlaGluGlyGly TyrValLeuTyr ProGlnIleGly AspArgLeuAsp LeuLeuCysPro

433 CGGGCCCGGCCT CCTGGCCCTCAC TCCTCTCCTAAT TATGAGTTCTAC AAGCTGTACCTG GTAGGGGGTGCT
    GCCCGGGCCGGA GGACCGGGAGTG AGGAGAGGATTA ATACTCAAGATG TTCGACATGGAC CATCCCCCACGA
 64 ArgAlaArgPro ProGlyProHis SerSerProAsn TryGluPheTyr LysLeuTyrLeu ValGlyGlyAla

505 CAGGGCCGGCGC TGTGAGGCACCC CCTGCCCCAAAC CTCCTTCTCACT TGTGATCGCCCA GACCTGGATCTC
    GTCCCGGCCGCG ACACTCCGTGGG GGACGGGGTTTG GAGGAAGAGTGA ACACTAGCGGGT CTGGACCTAGAG
 88 GlnGlyArgArg CysGluAlaPro ProAlaProAsn LeuLeuLeuThr CysAspArgPro AspLeuAspLeu

577 CGCTTCACCATC AAGTTCCAGGAG TATAGCCCTAAT CTCTGGGGCCAC GAGTTCCGCTCG CACCACGATTAC
    GCGAAGTGGTAG TTCAAGGTCCTC ATATCGGGATTA GAGACCCCGGTG CTCAAGGCGAGC GTGGTGCTAATG
112 ArgPheThrIle LysPheGlnGlu TyrSerProAsn LeuTrpGlyHis GluPheArgSer HisHisAspTyr
```

FIG. 2A

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649  TACATCATTGCC ACATCGGATGGG ACCCGGGAGGGC CTGGAGAGCCTG CAGGGAGGTGTG TGCCTAACCAGA
     ATGTAGTAACGG TGTAGCCTACCC TGGGCCCTCCCG GACCTCTCGGAC GTCCCTCCACAC ACGGATTGGTCT
136  TyrIleIleAla ThrSerAspGly ThrArgGluGly LeuGluSerLeu GlnGlyGlyVal CysLeuThrArg

721  GGCATGAAGGTG CTTCTCCGAGTG GGACAAAGTCCC CGAGGAGGGGCT GTCCCCCGAAAA CCTGTGTCTGAA
     CCGTACTTCCAC GAAGAGGCTCAC CCTGTTTCAGGG GCTCCTCCCCGA CAGGGGGCTTTT GGACACAGACTT
160  GlyMetLysVal LeuLeuArgVal GlyGlnSerPro ArgGlyGlyAla ValProArgLys ProValSerGlu

793  ATGCCCATGGAA AGAGACCGAGGG GCAGCCCACAGC CTGGAGCCTGGG AAGGAGAACCTG CCAGGTGACCCC
     TACGGGTACCTT TCTCTGGCTCCC CGTCGGGTGTCG GACCTCGGACCC TTCCTCTTGGAC GGTCCACTGGGG
184  MetProMetGlu ArgAspArgGly AlaAlaHisSer LeuGluProGly LysGluAsnLeu ProGlyAspPro

865  ACCAGCAATGCA ACCTCCCGGGGT GCTGAAGGCCCC CTGCCCCCTCCC AGCATGCCTGCA GTGGCTGGGGCA
     TGGTCGTTACGT TGGAGGGCCCCA CGACTTCCGGGG GACGGGGGAGGG TCGTACGGACGT CACCGACCCCGT
208  ThrSerAsnAla ThrSerArgGly AlaGluGlyPro LeuProProPro SerMetProAla ValAlaGlyAla

937  GCAGGGGGGCTG GCGCTGCTCTTG CTGGGCGTGGCA GGGGCTGGGGGT GCCATGTGTTGG CGGAGACGGCGG
     CGTCCCCCCGAC CGCGACGAGAAC GACCCGCACCGT CCCCGACCCCCA CGGTACACAACC GCCTCTGCCGCC
232  AlaGlyGlyLeu AlaLeuLeuLeu LeuGlyValAla GlyAlaGlyGly AlaMetCysTrp ArgArgArgArg

1009 GCCAAGCCTTCG GAGAGTCGCCAC CCTGGTCCTGGC TCCTTCGGGAGG GGAGGGTCTCTG GGCCTGGGGGGT
     CGGTTCGGAAGC CTCTCAGCGGTG GGACCAGGACCG AGGAAGCCCTCC CCTCCCAGAGAC CCGGACCCCCCA
256  AlaLysProSer GluSerArgHis ProGlyProGly SerPheGlyArg GlyGlySerLeu GlyLeuGlyGly

1081 GGAGGTGGGATG GGACCTCGGGAG GCTGAGCCTGGG GAGCTAGGGATA GCTCTGCGGGGT GGCGGGGCTGCA
     CCTCCACCCTAC CCTGGAGCCCTC CGACTCGGACCC CTCGATCCCTAT CGAGACGCCCCA CCGCCCCGACGT
280  GlyGlyGlyMet GlyProArgGlu AlaGluProGly GluLeuGlyIle AlaLeuArgGly GlyGlyAlaAla

1153 GATCCCCCCTTC TGCCCCCACTAT GAGAAGGTGAGT GGTGACTATGGG CATCCTGTGTAT ATCGTGCAGGAT
     CTAGGGGGGAAG ACGGGGGTGATA CTCTTCCACTCA CCACTGATACCC GTAGGACACATA TAGCACGTCCTA
304  AspProProPhe CysProHisTyr GluLysValSer GlyAspTyrGly HisProValTyr IleValGlnAsp

1225 GGGCCCCCCCAG AGCCCTCCAAAC ATCTACTACAAG GTATGAGGGCTC TTGGAGTGGCCC ATATTGCATACG
     CCCGGGGGGGTC TCGGGAGGTTTG TAGATGATGTTC CATACTCCCGAG AACCTCACCGGG TATAACGTATGC
328  GlyProProGln SerProProAsn IleTyrTyrLys ValOP* (SEQ ID NO: 4)
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FIG. 2B

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1297	AGCCCTTCTTGG	GGTGCTCCTCCA	GTTTAATTCCTG	GTTTGAGGGACA	CCTCTAACATCT	CGGCCCCCTGTG
	TCGGGAAGAACC	CCACGAGGAGGT	CAAATTAAGGAC	CAAACTCCCTGT	GGAGATTGTAGA	GCCGGGGGACAC
1369	CCCCCCCAGCCC	CTTCACTCCTCC	CGGCTGCTGTCC	TCGTCTCCACTT	TTAGGATTCCTT	AGGATTCCCACT
	GGGGGGGTCGGG	GAAGTGAGGAGG	GCCGACGACAGG	AGCAGAGGTGAA	AATCCTAAGGAA	TCCTAAGGGTGA
1441	GCCCCACTTCCT	GCCCTCCCGTTT	GGCCATGGGTGC	CCCCCTCTGTCT	CAGTGTCCCTGG	ATCCTTTTTCCT
	CGGGGTGAAGGA	CGGGAGGGCAAA	CCGGTACCCACG	GGGGGAGACAGA	GTCACAGGGACC	TAGGAAAAAGGA
1513	TGGGGAGGGGCA	CAGGCTCAGCCT	CCTCTCTGACCA	TGACCCAGGCAT	CCTTGTCCCCCT	CACCCACCCAGA
	ACCCCTCCCCGT	GTCCGAGTCGGA	GGAGAGACTGGT	ACTGGGTCCGTA	GGAACAGGGGGA	GTGGGTGGGTCT
1585	GCTAGGGGCGGG	AACAGCCCACCT	TTTGGTTGGCAC	CGCCTTCTTTCT	GCCTCTCACTGG	TTTTCTCTTCTC
	CGATCCCCGCCC	TTGTCGGGTGGA	AAACCAACCGTG	GCGGAAGAAAGA	CGGAGAGTGACC	AAAAGAGAAGAG
1657	TATCTCTTATTC	TTTCCCTCTCTT	CCGTCTCTAGGT	CTGTTCTTCTTC	CCTAGCATCCTC	CTCCCCACATCT
	ATAGAGAATAAG	AAAGGGAGAGAA	GGCAGAGATCCA	GACAAGAAGAAG	GGATCGTAGGAG	GAGGGGTGTAGA
1729	CCTTTCACCCTC	TTGGCTTCTTAT	CCTGTGCCTCTC	CCATCTCCTGGG	TGGGGGCATCAA	AGCATTTCTCCC
	GGAAAGTGGGAG	AACCGAAGAATA	GGACACGGAGAG	GGTAGAGGACCC	ACCCCCGTAGTT	TCGTAAAGAGGG
1801	CTTAGCTTTCAG	CCCCCCTTCTGA	CCTCTCATACCA	ACCACTCCCCTC	AGTCTGCCAAAA	ATGGGGGCCTTA
	GAATCGAAAGTC	GGGGGGAAGACT	GGAGAGTATGGT	TGGTGAGGGGAG	TCAGACGGTTTT	TACCCCCGGAAT
1873	TGGGGAAGGCTC	TGACACTCCACC	CCAGCTCAGGCC	ATGGGCACCAGG	GCTCCATTCTCT	GGCCTGGCCCAG
	ACCCCTTCCGAG	ACTGTGAGGTGG	GGTCGAGTCCGG	TACCCGTCGTCC	CGAGGTAAGAGA	CCGGACCGGGTC
1945	GCCTCTACATAC	TTACTCCAGCCA	TTTGGGGTGGTT	GGGTCATGACAG	CTACCATGAGAA	GAAGTGTCCCGT
	CGGAGATGTATG	AATGAGGTCGGT	AAACCCCACCAA	CCCAGTACTGTC	GATGGTACTCTT	CTTCACAGGGCA
2017	TTTGTCCSGTGG	CCAATAGCAAGA	TATGAACCGGTC	GGGACATGTATG	GACTTGGTCTGA	TGCTGAATGGGC
	AAACAGGTCACC	GGTTATCGTTCT	ATACTTGGCCAG	CCCTGTACATAC	CTGAACCAGACT	ACGACTTACCCG

FIG. 2C

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2089  CACTTGGGACCG GAAGTGACTTGC TCCAGACAAGAG GTGACCAGGCCC GGACAGAAATGG CCTGGGAAGTAG
      GTGAACCCTGGC CTTCACTGAACG AGGTCTGTTCTC CACTGGTCCGGG CCTGTCTTTACC GGACCCTTCATC

2161  CAGAAGCAGTGC AGCAGGAACTGG AAGTGCCTTCAT CCAGGACAGGAA GTAGCACTTCTG AAACAGGAAGTG
      GTCTTCGTCACG TCGTCCTTGACC TTCACGGAAGTA GGTCCTGTCCTT CATCGTGAAGAC TTTGTCCTTCAC

2233  GTCTGGCTGGAA CTCCAAGTGGCT TAGTCTGGGGGA TCAGGAGGTGGG AGGTGGATGGTT CTTATTCTGTGG
      CAGACCGACCTT GAGGTTCACCGA ATCAGACCCCCT AGTCCTCCACCC TCCACCTACCAA GAATAAGACACC

2305  AGAAGAAGGGCG GGAAGAACTTCC TTTCAGGAGGAA GCTGGAACTTAC TGACTGTAAGAG GTTAGAGGTGGA
      TCTTCTTCCCGC CCTTCTTGAAGG AAAGTCCTCCTT CGACCTTGAATG ACTGACATTCTC CAATCTCCACCT

2377  CCGA (SEQ ID NO: 3)
      GGCT
```

FIG. 2D

FIG. 2A
FIG. 2B
FIG. 2C
FIG. 2D

FIG. 2

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AL-2b.L    1 GNTCTAGAANTAGTGGATCCCCCGGGCTGCAGGAATTCCGACGGCCCCT
AL-2b.L   51 GGAAGGGCTCTGGTGGGGCTGAGCGCTCTGCCGCGGGGGCGCGGGCACAG
AL-2b.L  101 CAGGAAGCAGGTCCGCGTGGGCGCTGGGGGCATCAGCTACCGGGGTGGTC
AL-2b.L  151 CGGGCTGAAGAGCCAGGCAGCCAAGGCAGCCACCCCGGGGGGTGGGCGAC
AL-2b.L  201 TTTGGGGGAGTTGGTGCCCCGCCCCCCAGGCCTTGGCGGGGTCATGGGGC
AL-2b.L  251 CCCCCCATTCTGGGCCGGGGGGCGTGCGAGTCGGGGCCCTGCTGCTGCTG
AL-2b.L  301 GGGGTTTTGGGGCTGGTGTCTGGGCTCAGCCTGGAGCCTGTCTACTGGAA
AL-2b.L  351 CTCGGCGAATAAGAGGTTCCAGGCAGAGGGTGGTTATGTGCTGTACCCTC
AL-2b.L  401 AGATCGGGGACCGGCTAGACCTGCTCTGCCCCCGGGCCCGGCCTCCTGGC
AL-2b.L  451 CCTCACTCCTCTCCTAATTATGAGTTCTACAAGCTGTACCTGGTAGGGGG
AL-2b.L  501 TGCTCAGGGCCGGCGCTGTGAGGCACCCCCTGCCCCAAACCTCCTTCTCA
H10006     1 --------GCCGACGCTGTGAGGCACCCCCTGCCCCAAACCTCCTTCTCA
AL-2b.L  551 CTTGTGATCGCCCAGACCTGGATCTCCGCTTCACCATCAAGTTCCAGGAG
H10006    43 CTTGTGATCGCCCAGACCTGGATCTCCGCTTCACCATCAAGTTCCAGGAG
AL-2b.L  601 TATAGCCCTAATCTCTGGGGCCACGAGTTCCGCTCGCACCACGATTACTA
H10006    93 TATAGCCCTAATCTCTGGGGCCACGAGTTCCGCTCGCACCACGATTACTA
AL-2b.L  651 CATCATTGCCACATCGGATGGGACCCGGGAGGGCCTGGAGAGCCTGCAGG
H10006   143 CATCATTGCCACATCGGATGGGACCCGGGAGGCCTGGGAGAGCCTGCAGG
AL-2b.L  701 GAGGTGTGTGCCTAACCAGAGGCATGAAGGTGCTTCTCCGAGTGGGACAA
H10006   193 GAAGTGTGTGCCTAACCAGAGGCATGAAGGTGCTTCTCCGAGTNGGACAA
```

FIG. 3A

```
AL-2b.L  751  AGTCCCCGAGGAGGGGCTGTCCCCCGAAAACCTGTGTCTGAAATGCCCAT
H10006   243  AGT-CCCGAGGAGGGGCTGTCCCCCGAAAACCTGTGTCTGAAATGCCCAT

AL-2b.L  801  GGAAAGAGACCGAGGGGCAGCCCACAGCCT-GGAGCCT-GGGAAGGAGAA
H10006   292  GGAAAGAGACCGAGGGGCAGCCCACAGCCTGGGAGCCTGGGGAAGGAGAA

AL-2b.L  849  CCTGCCAGGTGACCCCACCAGCAATGCAACCTCCCGGGGT--GCTGAAGG
H10006   342  CCTGCCAGGTGACCCCACCAGCAATNCAACCTTCCGGGGTTGCTTGAAGG

AL-2b.L  897  CCCCCT--GCCCCCTCCCAGCA-TGCCTGCAGT--GGCTGGGGCAGCAGG
H10006   392  GCCCCTTGACCCTTTCCCAGCATTGCNTGCANTTGGTTNGGGGCAGCANG

AL-2b.L  942  GGGGC----TGGCGCTGCTCTTGCTGGGCGTGGCAGGGGCTGGGGGTGCC
H10006   442  GGGGNGTTTTGGC (SEQ ID NO: 5)

AL-2b.L  988  ATGTGTTGGCGGAGACGGCGGGCCAAGCCTTCGGAGAGTCGCCACCCTGG

AL-2b.L 1038  TCCTGGCTCCTTCGGGAGGGGAGGGTCTCTGGGCCTGGGGGGTGGAGGTG

AL-2b.L 1088  GGATGGGACCTCGGGAGGCTGAGCCTGGGGAGCTAGGGATAGCTCTGCGG

AL-2b.L 1138  GGTGGCGGGGCTGCAGATCCCCCCTTCTGCCCCCACTATGAGAAGGTGAG

AL-2b.L 1188  TGGTGACTATGGGCATCCTGTGTATATCGTGCAGGATGGGCCCCCCCAGA

AL-2b.L 1238  GCCCTCCAAACATCTACTACACATCGATTTCTGTGTTGGAGTGGCCCATA

AL-2b.L 1288  TTGCATACGATACAACTGTTTTTCATGCGATCCAAGTGCTCCCGTGTCAC
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FIG. 3B

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AL-2b.L 1338 T A C A T T C T T A T T T C C T G T G C A A G T T A T T A C G A C A T C G A C T T G C C G G A T G A
AL-2b.L 1388 C T T C A T T T A G C T T T A C G A C C C T G A A C C C A T C C A T G C A G G C C T G C A G A G C A
AL-2b.L 1438 C A G A T G G G G G A A T T C C G A A T C A G A T G G T G T T T C T G G G G G A C A G G A T C C T
AL-2b.L 1488 G G G T A C G G C T C T G T T T G T G C T T G T G C T T A T T C T T C T T C T T G G G A G G C T G A
AL-2b.L 1538 A T A T G C A T C A G A C G A C A G T G C T C C G G C A A C G G G C C A G T G T G G A G G C G G A A
AL-2b.L 1588 G C C G G C C A G C A T G G T C C G C T G T G A T A G G A T T G A A A G A G C T A C T G A G A A T A
AL-2b.L 1638 G G G G G C T T C T C A A T G A G A G A G C G G A G G C T G C T G T T A T C A T G G G A A C C A G G
AL-2b.L 1688 C A G A T C A A T C A T C C C T G G C A G Q T C A G G C A G G A A G T T A C T T A G C T T C T C C T
AL-2b.L 1738 T C A C C T T C T T C C C A C A G A A T T T A T T A T A G G C T T G T T C C A A G T T G T A G T G T
AL-2b.L 1788 G T G A T C A G A T T C G T G C T G C C T G T C A G C T C T G T G C T A C C T G G C A G T T C C C C
AL-2b.L 1838 T C A T G G A A T T C G A T A T C A A G C T T A T C G A T A C C G T C G A C C T (SEQ ID NO: 1)

FIG. 3C

FIG. 3A
FIG. 3B
FIG. 3C

FIG. 3

```
lerk2       1   MA-RPGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKG
huHTKL      1   MAVRRDSVWKYCWGVLMV---LCRTAISKSIVLEPIYWNSSNSKFLPGQG
AL2.sht     1   MG-PPHSGPGGVRVGALLLLGVLGLVSGL--SLEPVYWNSANKRFQAEGG
AL2.long    1   MG-PPHSGPGGVRVGALLLLGVLGLVSGL--SLEPVYWNSANKRFQAEGG

lerk2       50  LVIYPKIGDKLDIICPRA---EAGR--PYEYYKLYLVRPEQAAACSTVLD
huHTKL      48  LVLYPQIGDKLDIICPKV---DSKTVGQYEYYKVYMVDKDQADRCTIKKE
AL2.sht     48  YVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPA
AL2.long    48  YVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPA

lerk2       95  PNVLVTCNRPEQEIRFTIKFQEFSPNYMGLEFKKHHDYYITSTSNGSLEG
huHTKL      95  NTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNKDYYIISTSNGSLEG
AL2.sht     98  PNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREG
AL2.long    98  PNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREG

lerk2       145 LENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTTSRPSKEADNTVKMATQ
huHTKL      145 LDNQEGGVCQTRAMKILMKVGQDASS------AGSTRNKDPTRRPELEAG
AL2.sht     148 LESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLE
AL2.long    148 LESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLE
```

FIG. 4A

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lerk2      195 A P G S R G S L G D S D G K H E T V N Q E E K S G P G A S G G S S G D P D G F F N S K V A L F A A V
huHTKL     189 T N G - R S S T T S P F V K P N P G S S T D G N S A G H S G - - - - - - N N I L G S E V A L F A G I
AL2.sht    198 - P G K E N L P G D P T S N A T S R G A E G P L P P P S M P A V A G A A G G L - - - A L L L L G V A
AL2.long   198 - P G K E N L P G D P T S N A T S R G A E G P L P P P S M P A V A G A A G G L - - - A L L L L G V A

lerk2      245 G A G C V I F L L I I I F L T V L L L K L R K R H R K H T Q - Q R A A A L S L S T L A S P K G G S G
huHTKL     232 A S G C I I F I V I I I T L V V L L L K Y R R R H R K H S P - Q H T T T L S L S T L A T P K R S G N
AL2.sht    244 G A G G A - - - - - M C W R R R R A K P S E S R H P G P G S F G R G G S L G L G G - - - - G G G M G
AL2.long   244 G A G G A - - - - - M C W R R R R A K P S E S R H P G P G S F G R G G S L G L G G - - - - G G G M G

lerk2      294 T A G T E P S D I I I P L R - - - T T E N N Y C P H Y E K V S G D Y G H P V Y I V Q E M P P Q S P A
huHTKL     261 N N G S E P S D I I I P L R - - - T A D S V F C P H Y E K V S G D Y G H P V Y I V Q E M P P Q S P A
AL2.sht    265 P R E A E P G E L G I A L R G G G A A D P P F C P H Y E K V S G D Y G H P V Y I V Q D G P P Q S P P
AL2.long   295 P R E A E P G E L G I A L R G G G A A D P P F C P H Y E K V S G D Y G H P V Y I V Q D G P P Q S P P

lerk2      341 N I Y Y - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
huHTKL     328 N I Y Y - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
AL2.sht    335 N I Y Y - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
AL2.long   335 N I Y Y T S I S V L E W P I L H T I Q L F F M R S K C S R V T T F L F P V Q V I T T S T C R M T S F
```

FIG. 4B

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lerk2     345 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -[K V]- - - - - - - - - - - - - - - - (SEQ ID NO: 9)
huHTKL    332 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -[K V]- - - - - - - - - - - - - - - - (SEQ ID NO: 10)
AL2.sht   339 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -[K V]- - - - - - - - - - - - - - - - (SEQ ID NO: 4)
AL2.long  385 S F T T L N P S M Q A C R A Q M G E F R I R W C F W G D R I L G T A L F V L V L I L L L G R L N M H

AL2.long  435 Q T T L L R Q R A S V E A E A G Q H G P L (SEQ ID NO: 2)
```

FIG. 4C

FIG. 4A
FIG. 4B
FIG. 4C

FIG. 4

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```
LERK2      1  MA-RPGQRWLSKWLVAMVVLTLCRLATPLAKNLEPVSWSSLNPKFLSGKG
huHTKL     1  MAVRRDSVWKYCWGVLMV---LCRTAISKSIVLEPIYWNSSNSKFLPGQG
AL2.long   1  MGPPHSGP-GGVRVGALLL--LGVLGLVSGLSLEPVYWNSANKRFQAEGG

LERK2     50  LVIYPKIGDKLDIICPRA---EAGR--PYEYYKLYLVRPEQAAACSTVLD
huHTKL    48  LVLYPQIGDKLDIICPKV---DSKTVGQYEYYKVYMVDKDQADRCTIKKE
AL2.long  48  YVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPA

LERK2     95  PNVLVTCNKPHQEIRFTIKFQEFSPNYMGLEFKKYHDYYITSTSNGSLEG
huHTKL    95  NTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNKDYYIISTSNGSLEG
AL2.long  98  PNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREG

LERK2    145  LENREGGVCRTRTMKIVMKVGQDPNAVTPEQLTTSRPSKESDNTVKTATQ
huHTKL   145  LDNQEGGVCQTRAMKILMKVGQDASS------AGSTRNKDPTRRPELEAG
AL2.long 148  LESLQGGVCLTRGMKVLLRVGQSPRG------GAVPRKPVSEMPMERDRG

huHTKL   195  APGRGSQGDSDGKHETVNQEEKSGPGAGGGSGDSDSFFNSKVALFAAVG
AL2.sht  189  TNGRSSTTSPFVKPNPGSSTDGNSAGHSG------NNILGSEVALFAGIA
AL2.long 192  AAHSLEPGKENLPGDPTSNATSRGAE----------GPLPPPSMPAVAGAA
```

FIG. 5A

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LERK2     245 A G C V I F L L I I I F L T V L L L K L R K R H R K H T Q Q R A A A L S L - - - S T L A S P K G G S
huHTKL    233 S G C I I F I V I I I T L V V L L L K Y R R R H R K H S P Q H T T T L S L - - - S T L A T P K R S G
AL2.long  233 G G L A L L L L G V A G A G G A M C W R R R R A K P S E S R H P G P G S F G R G G S L G L G G G G G

LERK2     292 - G T A G T E P S D I I I P L R - - - T T E N N Y C P H Y E K V S G D Y G H P V Y I V Q E M P P Q S
huHTKL    280 - N N N G S E P S D I I I P L R - - - T A D S V F C P H Y E K V S G D Y G H P V Y I V Q E M P P Q S
AL2.long  283 M G P R E A E P G E L G I A L R G G G A A D P P F C P H Y E K V S G D Y G H P V Y I V Q D G P P Q S

LERK2     338 P A N I Y Y - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
huHTKL    326 P A N I Y Y - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
AL2.long  333 P P N I Y Y T S I S V L E W P I L H T I Q L F F M R S K C S R V T T F L F P V Q V I T T S T C R M T

LERK2     344 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - K V - - - - - - - - - - (SEQ ID NO: 9)
huHTKL    332 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - K V - - - - - - - - - - (SEQ ID NO: 10)
AL2.long  383 S F S F T T L N P S M Q A C R A Q M G E F R I R W C F W G D R I L G T A L F V L V L I L L L G R L N

AL2.long  433 M H Q T T L L R Q R A S V E A E A G Q H G P L (SEQ ID NO: 2)
```

FIG. 5B

FIG. 5A
FIG. 5B

FIG. 5